(ii) when operably linked to a transcribable sequence promotes transcription of the transcribable sequence in one or more cells of a *Musaceae* plant.

Cancel claim 4 without prejudice.

REMARKS

Reconsideration of this application and entry of the foregoing amendments are respectfully requested.

Claims 1 and 3 have been amended to define the invention with additional clarity and claim 4 has been cancelled. Support for the revisions of claims 1 and 3 can be found, for example, at page 13, lines 9-14, and at page 11, lines 19-23. That the claims have been revised should not be taken as an indication that Applicants agree with any view expressed by the Examiner. Rather, the revisions are offered merely to advance prosecution and Applicants reserve the right to pursue any deleted subject matter in a continuation application.

Pursuant to the Examiner's request, submitted herewith is a substitute specification. The specification provided herewith is merely a clean copy of the application as it would have been transmitted by the International Bureau.

Claims 1, 3, 4 and 6 to 19 stand rejected under 35 USC 112, first paragraph, as allegedly being non-enabled. withdrawal of the rejection is submitted to be in order for the reasons that follow.

The Examiner contends that undue experimentation would be required to make and use a BSV promoter having any sequence other than SEQ ID NO:2 on the basis that '*even sequences that are highly homologous as a consequence of close phylogenetic relationship or highly stringent hybridization conditions may not exhibit promoter function because a change in as few as a single nucleotide can alter or eliminate promoter function.*' The alleged lack of enablement arises from this perceived unpredictability.

Applicants respectfully submit that the reasoning put forward by the Examiner does not support the conclusion that the claims lack enablement. By the same rationale, any polynucleotide or polypeptide claim not limited to a specific sequence would lack enablement. This would constitute a *de facto* bar on the patentability of such claims. In fact, no such bar exists. In this regard, attention is directed to the following examples of patents that include claims that recite generic nucleotide or polypeptide sequences and that were obviously considered enabled: USP 6,489,541, USP 6,483,012, USP 6,476,296, USP

6,469,230, USP 6,437,219, USP 6,433,249, USP 6,429,358, USP 6,423,886, USP 6,388,171, USP 6,362,395 and USP 6,353,154.

The analysis of whether or not undue experimentation is required to make or use an invention does not involve a single simple factual determination of, for example, predictability, but rather requires a weighing many factual considerations (*In re Wands*, 858 F.2d at 737, 8 USPQ2d at 1404 (Fed. Cir. 1988)).

A skilled person in this field at the time the invention was made possessed a high level of skill and was experienced in DNA manipulations and gene expression. To determine whether a sequence from BSV possessed promoter activity, the skilled person could simply operably link the sequence to a reporter gene, such as GUS or GFP gene, and assay for a change in color or fluorescence. This is a simple procedure for a molecular biologist to perform and merely involves following the tried and tested protocols set out in Sambrook et al or Ausubel et al (see page 15, lines 21-22, or page 40, lines 25-26, of the present specification). The skilled person would be well placed to carry out such routine procedures.

The specification provides guidance for performing these experiments (see, for example, page 15, line 24, to page 20, line 27) and also provides working examples, both

of how to isolate a BSV promoter sequence (Example 1) and how to test it for activity (Example 2). There is, therefore, considerable direction and guidance in the specification that would enable the skilled person to make and use the invention.

The mere fact that a determination of promoter activity requires experimentation does not indicate a lack of enablement. *In re Wands* provides: *enablement is not precluded by the necessity for some experimentation such as routine screening*. Routine screening is, of course, precisely what the skilled person would be required to do to confirm promoter activity. Furthermore, *a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed* (*In re Wands*). In the present case, the experimentation is both routine and guided by the specification and would not put an undue burden on the skilled person.

The Examiner further alleges that a lack of enablement arises from undue experimentation that is required to select from the claimed genus those polynucleotides likely to have promoter function, prior to actual testing.

Given that testing promoter activity does not constitute undue experimentation, the skilled person has no reason to perform a 'selection' step as suggested by the Examiner. The skilled person can take a polypeptide within the claims and find out whether or not it has promoter activity without undue experimentation and this is all that is required for the claims to be enabled. A skilled person can make and use the invention using this approach without employing a 'prediction' step.

In fact, given the scope of the present claims, the 'prediction' of sequences that would have promoter activity is trivial. The claims cover polynucleotides of promoter sequences from BSV isolates. Contrary to the Examiner's assertion, both of these features contribute to the definition of the genus of polynucleotides covered by the claims and cannot be disregarded in considering enablement. In fact, in some circumstances, the features of activity and source alone can define allowable subject-matter. See, for example, recently issued patents USP 6,433,251, USP 6,232,526, USP 6,207,879, USP 6,051,753 and USP 6,037,524. The claimed polynucleotides are defined further as having a close structural relationship with SEQ ID NO:2, in terms of either % identity or hybridization.

The amount of prediction required to select an active promoter sequence is therefore trivial. A polynucleotide sequence from a BSV isolate that is closely structurally related to SEQ ID NO:2 can be predicted to be a promoter with a reasonable degree of certainty without detailed structural analysis. Activity can, of course, be confirmed without undue experimentation as described above.

A consideration of factors such as the quantity of experimentation needed, the amount of direction provided, the level of one of ordinary skill, the predictability in the art, the existence of working examples, the nature of the invention and the state of the prior art and breadth of the claims as set out above indicates that a skilled person would be able to make and use the invention as claimed without undue experimentation.

Reconsideration is requested.

Claims 1, 3, 4 and 6 to 19 stand rejected under 35 USC 112, first paragraph, as lacking written description. The rejection is traversed.

The Examiner contends that 'merely' defining a promoter in terms of source, activity and structural relationship to SEQ ID NO:2 does not meet the written description requirement.

However, a detailed analysis of the written description following the approach set out in the USPTO Written Description Guidelines and Training Examples (see, in particular examples 9 and 14), shows that one would, in fact, conclude from the specification that Applicants were in possession of the claimed invention, and the written description requirement is, therefore, met.

The Examiner correctly indicates that the species of SEQ ID NO:2 is within the genus of claim 1 (a). However, a polynucleotide of SEQ ID NO:2 is also at least 95% similar (in fact, it is 100% similar) to SEQ ID NO:2 and the species of SEQ ID NO:2 thus falls within the genus of claim 1(b). A polynucleotide of SEQ ID NO:2 will also hybridize under stringent conditions to its complementary sequence, so the species of SEQ ID NO:2 also falls within the genus of claim 3.

It is noted that the designation of a sequence as a BSV sequence provides a limitation that forms part of the definition of the genus as claimed. Sequences from other organisms fall outside this definition and the genus of BSV promoter sequences is, therefore, smaller than the genus of promoter sequences generally. Assessment of whether a number of species is representative of a genus requires the genus to be correctly identified. Written description

cannot be correctly assessed if the feature of BSV origin in the definition of the genus is disregarded.

Claim 1 covers polynucleotides having SEQ ID NO:2 or having at least 95% identity to SEQ ID NO:2 which have promoter activity.

Procedures for either synthesising or isolating polynucleotides having at least 95% identity SEQ ID NO:2 are conventional in the art and methods are described and exemplified for identifying and isolating BSV promoter sequences (Example 1) and testing their activity (Example 2).

There is a single species disclosed that is within the scope of the claimed genus, that species being SEQ ID NO:2 and there is actual reduction to practice of the single disclosed species.

The specification indicates that the genus of promoters which are at least 95% identical to SEQ ID NO:2 does not have substantial variation since all of the variants must possess the specified promoter activity, must have at least 95% identity to the reference sequence, SEQ ID NO:2, and must be BSV sequences. The single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference sequence and because of the presence of a method

that Applicants provided and exemplified for identifying all of the BSV polynucleotides at least 95% identical to SEQ ID NO:2 that are capable of the specified promoter activity.

In view of the foregoing, it should be clear that Applicants were in possession of the necessary common attributes possessed by the members of the genus defined in claim 1.

Claim 3 is drawn to a genus of BSV polynucleotides all of which must selectively hybridize with SEQ ID NO:2 under specified highly stringent conditions and must have promoter activity in *Musaceae* cells.

The art indicates that hybridization techniques using a known DNA as a probe under highly stringent conditions were conventional in the art at the time of filing.

There is a single species disclosed (a molecule consisting of SEQ ID NO:2) that is within the scope of the claimed genus and there is actual reduction to practice of the disclosed species.

Now turning to the genus analysis, a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claim because the highly stringent hybridization conditions set forth in

the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed.

The disclosure therefore meets the requirements of 35 USC §112, first paragraph, as providing an adequate written description for the claimed invention. Reconsideration is requested.

Claims 3 to 20 stand rejected under 35 USC 102(e) over Olszewski et al in the light of Lockhart et al and Regenmortel et al. The rejection is traversed.

Claim 3 has been amended to specify that the promoter is a BSV promoter and the hybridization conditions have been modified based on page 11, lines 19-23, so that only sequences of greater than about 90% identity hybridize. Given that ScBV is only 51.2% homologous to BSV, and it has previously been shown that ScBV and BSV are distinct species, the disclosure of Olszewski et al falls outside the present claims.

Claim 3 as presently worded specifies an active promoter that hybridizes under stringent conditions to SEQ ID NO:2. The features provide a *de facto* lower limit to the size of the claimed sequences, as if they must be active and have greater than 90% identity with SEQ ID NO:2. Short, non-distinctive fragments of sequence fulfil neither of these criteria.

Reconsideration is requested.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned "**Version With Markings To Show Changes Made**."

This application is submitted to be in condition for allowance and a Notice to that effect is requested.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

1. (Twice Amended) An isolated polynucleotide consisting of a Banana Streak Virus promoter sequence selected from:

(a) the promoter sequence of a Nigerian isolate of Banana Streak Virus shown in SEQ ID [NO. 2] NO:2;

(b) a promoter sequence of an isolate of Banana Streak Virus[, which promoter sequence is an allelic variant of the promoter sequence of SEQ ID NO. 2; wherein said allelic variant has] having a sequence that is at least [75%] 95% identical to the promoter sequence of SEQ ID NO:2, p13

[(c)a fragment of] wherein said promoter sequence of (a) or (b) [which,] when operably linked to a transcribable sequence, promotes transcription of the transcribable sequence in one or more cells of a *Musaceae* plant.

3. (Twice Amended) An isolated polynucleotide consisting of a Banana Streak Virus promoter sequence, which promoter sequence:

(i) selectively hybridizes under stringent conditions with a polynucleotide complementary to a polynucleotide

which has the nucleotide sequence shown in SEQ ID [NO: 2] NO:2;

wherein said stringent conditions comprise overnight hybridization at [42°C] 65°C in 0.25M Na_2HPO_4, pH 7.2, 6.5% SDS, 10% dextran sulfate and a final wash at [55 °C] 60°C in 0.1x SSC, 0.1% SDS, and;

(ii) when operably linked to a transcribable sequence promotes transcription of the transcribable sequence in one or more cells of a *Musaceae* plant.